



SEQUENCE LISTING

<110> Kloek, Andrew
Williams, Deryck Jeremy
Salmon, Brandy Leigh

<120> NEMATODE MDH-LIKE SEQUENCE

<130> 12557-002001

<140> US 10/060,848

<141> 2002-01-30

<150> US 60/266,037

<151> 2001-02-02

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1327

<212> DNA

<213> Meloidogyne incognita

<220>

<221> CDS

<222> (55)...(1152)

<221> misc_feature

<222> (1)...(1327)

<223> n = A,T,C or G

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Asn Tyr Ser Lys Asp Ala Pro Glu Phe Val Val Ser Pro Lys Asp Ala
5 10 15

cgc gaa ttt gtt gta aaa tgt atg caa aca gtt gga aca tcc cct gac 153
Arg Glu Phe Val Val Lys Cys Met Gln Thr Val Gly Thr Ser Pro Asp
20 25 30

cat gct ggt caa tta gca gat cta tta ttg gat gct gat ctt gtt gga 201
His Ala Gly Gln Leu Ala Asp Leu Leu Leu Asp Ala Asp Leu Val Gly
35 40 45

cac tat agt cat ggt cta aat cga ctt cat att tat gtg gat gac gtc 249
His Tyr Ser His Gly Leu Asn Arg Leu His Ile Tyr Val Asp Asp Val
50 55 60 65

aaa aac gga gtt aaa gga aat gga gtt cca aaa gtg tta aaa caa aaa 297
Lys Asn Gly Val Lys Gly Asn Gly Val Pro Lys Val Leu Lys Gln Lys
70 75 80

gga ggc act gct tgg gtt gat gga gaa aat ctt ctg ggt gca gtt gtt Gly Gly Thr Ala Trp Val Asp Gly Glu Asn Leu Leu Gly Ala Val Val 85 90 95	345
gga aac ttc tgt acc gac ttg gct att aaa ttg gct aaa gaa ttt ggc Gly Asn Phe Cys Thr Asp Leu Ala Ile Lys Leu Ala Lys Glu Phe Gly 100 105 110	393
gtt gct tgg gtg gta aca aaa aat tct aat cat tat gga gct tgt caa Val Ala Trp Val Val Thr Lys Asn Ser Asn His Tyr Gly Ala Cys Gln 115 120 125	441
cat tat act aag aaa att gca aat gca gga atg gtg gga atg tct ttt His Tyr Thr Lys Lys Ile Ala Asn Ala Gly Met Val Gly Met Ser Phe 130 135 140 145	489
aca aat aca tcg cct ctc atg ttc ccc tgc cga tct tct gag att gga Thr Asn Thr Ser Pro Leu Met Phe Pro Cys Arg Ser Ser Glu Ile Gly 150 155 160	537
ctt ggt aca aac cct ctt tct tgt tgt gtc aac tcg gaa aag aca gga Leu Gly Thr Asn Pro Leu Ser Cys Cys Val Asn Ser Glu Lys Thr Gly 165 170 175	585
gac agt ttt ttg tta gac atg gct acg aca act gtt gct ctt gga aag Asp Ser Phe Leu Leu Asp Met Ala Thr Thr Thr Val Ala Leu Gly Lys 180 185 190	633
gta gag ctg gca gat tgt cgc ggt aaa aca caa att ccc tcc aca tgg Val Glu Leu Ala Asp Cys Arg Gly Lys Thr Gln Ile Pro Ser Thr Trp 195 200 205	681
ggt gcc gat tct aaa ggc aat cca tcg act gat aca caa gtt gtt tta Gly Ala Asp Ser Lys Gly Asn Pro Ser Thr Asp Thr Gln Val Val Leu 210 215 220 225	729
cac ggt ggc gga ctt ttg cct tta ggc ggt ata gaa gag acg gga tct His Gly Gly Gly Leu Leu Pro Leu Gly Gly Ile Glu Glu Thr Gly Ser 230 235 240	777
tac aaa gga acg ggt ctt tca atg atg ggt gaa ttg ttt tgt gga att Tyr Lys Gly Thr Gly Leu Ser Met Met Gly Glu Leu Phe Cys Gly Ile 245 250 255	825
ttg gca ggg tca agt ttt gga aaa aat gta cga tta tgg ggg caa tca Leu Ala Gly Ser Ser Phe Gly Lys Asn Val Arg Leu Trp Gly Gln Ser 260 265 270	873
cac aaa gcc gct gac aat ggc caa tgt ttt gtt gct att gat caa gaa His Lys Ala Ala Asp Asn Gly Gln Cys Phe Val Ala Ile Asp Gln Glu 275 280 285	921
tgt ttt gcc cca gga ttt gct cct cgt tta caa caa ttt ttg gat gaa Cys Phe Ala Pro Gly Phe Ala Pro Arg Leu Gln Gln Phe Leu Asp Glu 290 295 300 305	969

aca cgg aat ttg aaa ccg att tct gaa gaa aag cct gtt cta gtg cct 1017
 Thr Arg Asn Leu Lys Pro Ile Ser Glu Glu Lys Pro Val Leu Val Pro
 310 315 320

gga gat cct gaa aga atg aat aca gaa tat agc caa aag gct gga ggt 1065
 Gly Asp Pro Glu Arg Met Asn Thr Glu Tyr Ser Gln Lys Ala Gly Gly
 325 330 335

ttg gta tac caa gaa ggg cag ata aaa gct ttg gaa gag ttg gcc aca 1113
 Leu Val Tyr Gln Glu Gly Gln Ile Lys Ala Leu Glu Glu Leu Ala Thr
 340 345 350

aaa tgt gat gtt caa atg ttc tca tac aaa cga cta aaa tgaggatgag 1162
 Lys Cys Asp Val Gln Met Phe Ser Tyr Lys Arg Leu Lys
 355 360 365

atttaaatat ttttttgtgt agctgaaact gacttcaaac gagaaatgaa caatttccta 1222
 aaaagcagtt agataagggt ttatttttca tttattttatt ttttaacctc attttttata 1282
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<210> 2

<211> 2088

<212> DNA

<213> Meloidogyne incognita

<220>

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<222> (28)...(1125)

<221> misc_feature

<222> (1)...(2088)

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ttt gtt gtc tct cca aaa gat gct cgc gaa ttt gtt gta aaa tgt atg 102
 Phe Val Val Ser Pro Lys Asp Ala Arg Glu Phe Val Val Lys Cys Met
 10 15 20 25

caa aca gtt gga aca tcc cct gac cat gct ggt caa tta gca gat ctc 150
 Gln Thr Val Gly Thr Ser Pro Asp His Ala Gly Gln Leu Ala Asp Leu
 30 35 40

tta tta gat gct gat ctt gtt ggg cat tac agt cat ggt cta aat cgg 198
 Leu Leu Asp Ala Asp Leu Val Gly His Tyr Ser His Gly Leu Asn Arg
 45 50 55

ctt cat att tat gtg gat gac gtc aaa aat gga gtt aaa gga aat gga 246
 Leu His Ile Tyr Val Asp Asp Val Lys Asn Gly Val Lys Gly Asn Gly
 60 65 70

gtt cca aaa gtg tta aaa caa aaa gga ggc act gct tgg gtg gat gga 294
 Val Pro Lys Val Leu Lys Gln Lys Gly Gly Thr Ala Trp Val Asp Gly
 75 80 85

gaa aat ctt ttg ggt gca gtt gtt ggc aac ttc tgt acc gat ttg gct Glu Asn Leu Leu Gly Ala Val Val Gly Asn Phe Cys Thr Asp Leu Ala 90 95 100 105	342
att aaa ttg gct aaa gaa ttt ggt gtt gct tgg gtg gta aca aaa aat Ile Lys Leu Ala Lys Glu Phe Gly Val Ala Trp Val Val Thr Lys Asn 110 115 120	390
tct aat cat tat gga gct ngf caa cat tat act aag aaa att gcg aat Ser Asn His Tyr Gly Ala Xaa Gln His Tyr Thr Lys Lys Ile Ala Asn 125 130 135	438
gca gga atg gtg gga atg tca ttt aca aat act tca cct ctc atg ttc Ala Gly Met Val Gly Met Ser Phe Thr Asn Thr Ser Pro Leu Met Phe 140 145 150	486
ccc tgc cgt tct tct gag atc gga cta ggc aca aac cct ctt tct tgt Pro Cys Arg Ser Ser Glu Ile Gly Leu Gly Thr Asn Pro Leu Ser Cys 155 160 165	534
tgt gcc aac tcg gaa aag aca gaa gac agt ttt ttg tta gac atg gct Cys Ala Asn Ser Glu Lys Thr Glu Asp Ser Phe Leu Leu Asp Met Ala 170 175 180 185	582
act aca act gtt gct cta gga aag gtt gag ctg gca aat tgt cgc ggt Thr Thr Thr Val Ala Leu Gly Lys Val Glu Leu Ala Asn Cys Arg Gly 190 195 200	630
aaa aca caa att ccc tca gca tgg ggt gcc gat tct aaa ggc aat cca Lys Thr Gln Ile Pro Ser Ala Trp Gly Ala Asp Ser Lys Gly Asn Pro 205 210 215	678
tca aca gac aca caa gtt gtt tta cat ggt ggc gga ctt ttg cct tta Ser Thr Asp Thr Gln Val Val Leu His Gly Gly Gly Leu Leu Pro Leu 220 225 230	726
ggc ggt ata gaa gag acg gga tct tac aaa gga acg ggt ctc tca atg Gly Gly Ile Glu Glu Thr Gly Ser Tyr Lys Gly Thr Gly Leu Ser Met 235 240 245	774
atg ggt gaa ttg ttt tgt gga att ttg gca ggg tca agt ttt gga aaa Met Gly Glu Leu Phe Cys Gly Ile Leu Ala Gly Ser Ser Phe Gly Lys 250 255 260 265	822
aat gta cga tta tgg ggg caa tca cac aaa gcc gct gac aat ggc caa Asn Val Arg Leu Trp Gly Gln Ser His Lys Ala Ala Asp Asn Gly Gln 270 275 280	870
tgt ttt gtt gct att gat caa gaa tgt ttt gcc cca gga ttt gct cct Cys Phe Val Ala Ile Asp Gln Glu Cys Phe Ala Pro Gly Phe Ala Pro 285 290 295	918
cgt tta caa caa ttt ttg gat gaa aca cgg aat ttg aaa ccg att tct Arg Leu Gln Gln Phe Leu Asp Glu Thr Arg Asn Leu Lys Pro Ile Ser 300 305 310	966

gaa gaa aag cct gtt cta gtg cct gga gat cct gaa aga atg aat aca 1014
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 315 320 325

gaa tat agc caa aag gct gga ggt ttg gta tac caa gaa ggg cag ata 1062
 Glu Tyr Ser Gln Lys Ala Gly Gly Leu Val Tyr Gln Glu Gly Gln Ile
 330 335 340 345

aaa gct ttg gaa gag ttg gcc aca aaa tgt gat gtt caa atg ttc tca 1110
 Lys Ala Leu Glu Glu Leu Ala Thr Lys Cys Asp Val Gln Met Phe Ser
 350 355 360

tac aaa cga cta aaa tgaggatgag atttaaatat ttttttgtgt agctgaaact 1165
 Tyr Lys Arg Leu Lys
 365

gacttcaaac gagaaatgaa caatttctcta aaaagcagtt agataagggt ttattttttca 1225
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 tagnttttat aaattttaag agctgataga aaaatttagt tttgnaattt ttgaagaata 2005
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<210> 3

<211> 366

<212> PRT

<213> Meloidogyne incognita

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 Asp His Ala Gly Gln Leu Ala Asp Leu Leu Leu Asp Ala Asp Leu Val
 35 40 45
 Gly His Tyr Ser His Gly Leu Asn Arg Leu His Ile Tyr Val Asp Asp
 50 55 60
 Val Lys Asn Gly Val Lys Gly Asn Gly Val Pro Lys Val Leu Lys Gln
 65 70 75 80
 Lys Gly Gly Thr Ala Trp Val Asp Gly Glu Asn Leu Leu Gly Ala Val
 85 90 95
 Val Gly Asn Phe Cys Thr Asp Leu Ala Ile Lys Leu Ala Lys Glu Phe
 100 105 110
 Gly Val Ala Trp Val Val Thr Lys Asn Ser Asn His Tyr Gly Ala Cys
 115 120 125
 Gln His Tyr Thr Lys Lys Ile Ala Asn Ala Gly Met Val Gly Met Ser
 130 135 140

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Phe Thr Asn Thr Ser Pro Leu Met Phe Pro Cys Arg Ser Ser Glu Ile
145          150          155          160
Gly Leu Gly Thr Asn Pro Leu Ser Cys Cys Val Asn Ser Glu Lys Thr
          165          170          175
Gly Asp Ser Phe Leu Leu Asp Met Ala Thr Thr Thr Val Ala Leu Gly
          180          185          190
Lys Val Glu Leu Ala Asp Cys Arg Gly Lys Thr Gln Ile Pro Ser Thr
          195          200          205
Trp Gly Ala Asp Ser Lys Gly Asn Pro Ser Thr Asp Thr Gln Val Val
          210          215          220
Leu His Gly Gly Gly Leu Leu Pro Leu Gly Gly Ile Glu Glu Thr Gly
225          230          235          240
Ser Tyr Lys Gly Thr Gly Leu Ser Met Met Gly Glu Leu Phe Cys Gly
          245          250          255
Ile Leu Ala Gly Ser Ser Phe Gly Lys Asn Val Arg Leu Trp Gly Gln
          260          265          270
Ser His Lys Ala Ala Asp Asn Gly Gln Cys Phe Val Ala Ile Asp Gln
          275          280          285
Glu Cys Phe Ala Pro Gly Phe Ala Pro Arg Leu Gln Gln Phe Leu Asp
          290          295          300
Glu Thr Arg Asn Leu Lys Pro Ile Ser Glu Glu Lys Pro Val Leu Val
305          310          315          320
Pro Gly Asp Pro Glu Arg Met Asn Thr Glu Tyr Ser Gln Lys Ala Gly
          325          330          335
Gly Leu Val Tyr Gln Glu Gly Gln Ile Lys Ala Leu Glu Glu Leu Ala
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Thr Lys Cys Asp Val Gln Met Phe Ser Tyr Lys Arg Leu Lys
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<210> 4

<211> 366

<212> PRT

<213> Meloidogyne incognita

<220>

<221> VARIANT

<222> (1)...(366)

<223> Xaa = Any Amino Acid

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          35          40          45
Gly His Tyr Ser His Gly Leu Asn Arg Leu His Ile Tyr Val Asp Asp
          50          55          60
Val Lys Asn Gly Val Lys Gly Asn Gly Val Pro Lys Val Leu Lys Gln
          65          70          75          80
Lys Gly Gly Thr Ala Trp Val Asp Gly Glu Asn Leu Leu Gly Ala Val
          85          90          95
Val Gly Asn Phe Cys Thr Asp Leu Ala Ile Lys Leu Ala Lys Glu Phe
          100          105          110
Gly Val Ala Trp Val Val Thr Lys Asn Ser Asn His Tyr Gly Ala Xaa
          115          120          125

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Gln His Tyr Thr Lys Lys Ile Ala Asn Ala Gly Met Val Gly Met Ser
 130 135 140
 Phe Thr Asn Thr Ser Pro Leu Met Phe Pro Cys Arg Ser Ser Glu Ile
 145 150 155 160
 Gly Leu Gly Thr Asn Pro Leu Ser Cys Cys Ala Asn Ser Glu Lys Thr
 165 170 175
 Glu Asp Ser Phe Leu Leu Asp Met Ala Thr Thr Thr Val Ala Leu Gly
 180 185 190
 Lys Val Glu Leu Ala Asn Cys Arg Gly Lys Thr Gln Ile Pro Ser Ala
 195 200 205
 Trp Gly Ala Asp Ser Lys Gly Asn Pro Ser Thr Asp Thr Gln Val Val
 210 215 220
 Leu His Gly Gly Gly Leu Leu Pro Leu Gly Gly Ile Glu Glu Thr Gly
 225 230 235 240
 Ser Tyr Lys Gly Thr Gly Leu Ser Met Met Gly Glu Leu Phe Cys Gly
 245 250 255
 Ile Leu Ala Gly Ser Ser Phe Gly Lys Asn Val Arg Leu Trp Gly Gln
 260 265 270
 Ser His Lys Ala Ala Asp Asn Gly Gln Cys Phe Val Ala Ile Asp Gln
 275 280 285
 Glu Cys Phe Ala Pro Gly Phe Ala Pro Arg Leu Gln Gln Phe Leu Asp
 290 295 300
 Glu Thr Arg Asn Leu Lys Pro Ile Ser Glu Glu Lys Pro Val Leu Val
 305 310 315 320
 Pro Gly Asp Pro Glu Arg Met Asn Thr Glu Tyr Ser Gln Lys Ala Gly
 325 330 335
 Gly Leu Val Tyr Gln Glu Gly Gln Ile Lys Ala Leu Glu Glu Leu Ala
 340 345 350
 Thr Lys Cys Asp Val Gln Met Phe Ser Tyr Lys Arg Leu Lys
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<210> 5

<211> 1098

<212> DNA

<213> Meloidogyne incognita

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ctattattgg	atgctgatct	tggtggacac	tatagtcatg	gtctaaatcg	acttcatatt	180
tatgtggatg	acgtcaaaaa	cggagttaaa	ggaaatggag	ttccaaaagt	gttaaaacaa	240
aaaggaggca	ctgcttgggt	tgatggagaa	aatcttcttg	gtgcagttgt	tggaaacttc	300
tgtaccgact	tggtatttaa	attggctaaa	gaatttggcg	ttgcttgggt	ggtaacaaaa	360
aattctaata	attatggagc	ttgtcaacat	tatactaaga	aaattgcaaa	tgcaggaatg	420
gtgggaatgt	cttttacaaa	tacatgcct	ctcatgttcc	cctgccgatc	ttctgagatt	480
ggacttggta	caaaccctct	ttcttgttgt	gtcaactcgg	aaaagacagg	agacagtttt	540
ttgttagaca	tggtacgac	aactgttgct	cttggaaagg	tagagctggc	agattgtcgc	600
ggtaaaacac	aaattccctc	cacatggggt	gccgattcta	aaggcaatcc	atcgactgat	660
acacaagttg	ttttacacgg	tggcggactt	ttgccttttag	gcggtataga	agagacggga	720
tcttacaaag	gaacgggtct	ttcaatgatg	ggtgaattgt	tttgtggaat	tttggcaggg	780
tcaagttttg	gaaaaaatgt	acgattatgg	gggcaatcac	acaaagccgc	tgacaatggc	840
caatgttttg	ttgctattga	tcaagaatgt	tttgccccag	gatttgctcc	tcgttttacaa	900
caatttttgg	atgaaacacg	gaatttgaaa	ccgattttctg	aagaaaagcc	tgttctagtg	960
cctggagatc	ctgaaagaat	gaatacagaa	tatagccaaa	aggctggagg	tttgggtatac	1020
caagaagggc	agataaaaagc	tttggaagag	ttggccacaa	aatgtgatgt	tcaaattgttc	1080
tcatacaaac	gactaaaa					1098

<210> 6
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 <212> DNA
 <213> Meloidogyne incognita

<220>
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 <222> (1)...(1098)
 <223> n = A,T,C or G

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 ctcttattag atgctgatct tggtgggcat tacagtcattg gtctaaatcg gcttcatatt 180
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 aattctaate attatggagc tngtcaacat tatactaaga aaattgcaa tgcaggaatg 420
 gtgggaatgt catttacaaa tacttcacct ctcatgttcc cctgccgttc ttctgagatc 480
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 tcaagttttg gaaaaaatgt acgattatgg gggcaatcac acaaagccgc tgacaatggc 840
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 caatttttgg atgaaacacg gaatttgaaa ccgatttctg aagaaaagcc tgttctagtg 960
 cctggagatc ctgaaagaat gaatacagaa tatagccaaa aggctggagg tttggtatag 1020
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 <213> Caenorhabditis elegans

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 35 40 45
 Cys Ser Asp Tyr Arg Gly His Tyr Ser His Gly Ile Asn Arg Leu His
 50 55 60
 Ile Tyr Val His Asp Leu Met Met Lys Ser Thr Ala Val Thr Gly Thr
 65 70 75 80
 Pro Gln Val Leu Lys Ser Lys Gly Ser Thr Ala Trp Val Asp Gly Asn
 85 90 95
 Asn Leu Leu Gly Pro Val Val Gly Asn Phe Cys Met Gln Leu Ala Val
 100 105 110
 Glu Lys Ala Lys Glu Phe Gly Ile Gly Trp Val Val Cys Arg Asn Ser
 115 120 125
 Asn His Phe Gly Ile Ala Gly Trp Tyr Ala Asp Phe Ala Cys Arg Asn
 130 135 140
 Gly Leu Val Gly Met Ala Phe Thr Asn Thr Ser Pro Cys Val Phe Pro
 145 150 155 160


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Thr Gly Ser Arg Glu Lys Ser Leu Gly Ser Asn Pro Ile Cys Met Ala
      165      170      175
Ala Pro Gly Met Glu Gly Asp Ser Phe Phe Leu Asp Met Ala Ser Thr
      180      185      190
Thr Val Ala Tyr Gly Lys Ile Glu Val Val Asp Arg Lys Gly Glu Thr
      195      200      205
Tyr Ile Pro Gly Ser Trp Gly Ala Asp Lys Asn Gly Asp Glu Thr His
      210      215      220
Asn Pro Lys Glu Val Leu Asp Gly Gly Gly Leu Gln Pro Leu Gly Gly
      225      230      235      240
Ser Glu Ile Thr Gly Gly Tyr Lys Gly Thr Gly Leu Cys Met Met Val
      245      250      255
Glu Val Leu Cys Gly Ile Met Gly Gly Ser Ala Phe Gly Lys Asn Ile
      260      265      270
Arg Gln Trp Gln Thr Thr Ser Lys Thr Ala Asp Leu Gly Gln Cys Phe
      275      280      285
Val Ala Ile Asp Pro Glu Cys Phe Ala Pro Gly Phe Ser Asn Arg Leu
      290      295      300
Gln Glu Phe Cys Asp Glu Thr Arg Asn Leu Asn Pro Ile Asn Pro Ser
      305      310      315      320
Arg Pro Pro Gln Val Pro Gly Asp Pro Glu Arg Ala His Met Asn Met
      325      330      335
Cys Asp Asp Leu Gly Gly Ile Val Tyr Lys Lys Lys Gln Leu Asp His
      340      345      350
Leu Lys Asn Leu Ala Asp Arg Leu Gly Val Ile Met Arg Leu Val Asp
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Glu Lys Pro Gln
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<210> 8

<211> 400

<212> PRT

<213> Caenorhabditis elegans

<400> 8

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Phe Tyr Ser Thr Thr Asp Asp Asn Met Ala Ala Pro Glu Glu Ser Val
      35      40      45
Val Ala Lys Asp Glu Met Lys Arg Phe Met Val Glu Cys Met Thr Lys
      50      55      60
Val Gly Ala Thr Glu Ser His Ala Thr Gln Leu Ala Leu Val Leu Leu
      65      70      75      80
Glu Gly Asp Ile Arg Gly His Tyr Ser His Gly Leu Asn Arg Leu Asp
      85      90      95
Met Tyr Val Arg Asp Ile Glu Gln Asn Val Cys Lys Gly Asp Gly Glu
      100      105      110
Pro Ile Ile Leu Lys Glu Lys Ala Gly Thr Ala Trp Val Asp Gly Asn
      115      120      125
Asn Leu Leu Gly Pro Val Val Gly Asn Phe Cys Met Asp Leu Ala Ile
      130      135      140
Glu Lys Ala Lys Asn Ala Gly Ile Gly Trp Val Val Ala Lys Gly Ser
      145      150      155      160
Asn His Tyr Gly Ile Ala Gly Trp Tyr Ala Leu Arg Ala Met Lys Lys
      165      170      175

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Gly Met Leu Gly Met Ser Met Thr Asn Thr Ser Pro Ile Ser Phe Pro
 180 185 190
 Thr Arg Ser Ala Val Pro Ala Leu Gly Thr Asn Pro Ile Ser Leu Ala
 195 200 205
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 210 215 220
 Thr Val Ala Ile Gly Lys Val Glu Leu Ala Ala Arg Lys Glu Asn Pro
 225 230 235 240
 Val Pro Leu Ser Trp Gly Val Gly Glu Gly Lys Glu Thr Thr Asp
 245 250 255
 Pro Thr Lys Val Leu Tyr Gly Gly Gly Leu Leu Pro Leu Gly Gly Val
 260 265 270
 Glu Val Ser Gly Gly Tyr Lys Gly Tyr Gly Leu Ser Ser Met Ile Glu
 275 280 285
 Ile Phe Cys Gly Ile Leu Ala Gly Ala His Trp Gly Pro His Val Arg
 290 295 300
 Lys Trp Met Ser Thr Lys Ser Glu Ala Asp Leu Gly Gln Cys Phe Val
 305 310 315 320
 Ala Ile Asp Pro Glu Ala Phe Ala Pro Gly Phe Ala Asp Arg Leu Gln
 325 330 335
 Asp Phe Met Gln Thr Met Arg Ala Leu Pro Thr Ser Ser Pro Ser Phe
 340 345 350
 Lys Val Glu Val Ala Gly Asp Met Glu Arg Arg His Glu Ala Leu Val
 355 360 365
 Glu Gln Leu Gly Gly Ile Pro Tyr His Lys Asn Gln Ile Thr Phe Val
 370 375 380
 Asn Asp Leu Ala Ala Lys Leu Gly Val Lys Thr Val Asp Leu Val Gln
 385 390 395 400

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